

SECTION I

RELEASE OF CAPTIVE-BRED SPECIES: NON-TECHNICAL REVIEW

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**1 INTRODUCTION**

1.1 Plants and animals bred in captivity have been deliberately released into the wild for several reasons, including

- a. restoration of a species to an area or habitat from which it has been lost;
- b. augmenting populations which have reached low numbers;
- c. improving the genetic diversity of populations or introducing certain desirable traits;
- d. introduction of a new species to improve the biological diversity of an area;
- e. provision of a population for future harvesting or sport;
- f. biological control of pest species including weeds.

Releases for reasons a-d commonly have a nature conservation objective, and reasons a-e have been given for releasing captive-bred species of fish, gamebirds and deer. In addition, a large number of captive-bred organisms have been introduced into the wild accidentally, usually as escapes from domestication or cultivation. Well-known examples of escapes in Britain include the South American coypu and the North American mink.

1.2 This report focuses on a specific aspect of the release of captive-bred organisms: viz. the likelihood and implications of genetic interaction between released individuals and individuals from the same or related species occurring naturally in the wild.

Such interaction could occur by hybridisation between released individuals, or their descendants, and wild individuals, or, in microorganisms, by transformation, transduction or conjugation. There is general concern over the possibility that hybridisation between captive-bred and naturally-occurring individuals may have detrimental genetic effects. These could occur by introducing unfavourable or undesirable genes, reducing the genetic diversity of natural populations, replacing locally-differentiated populations by genetic swamping, or reducing individual fitness and thus threatening survival. All these possibilities have important implications for wildlife conservation and should be considered in the planning of future releases for conservation purposes.

1.3 Our approach to this problem has been to review the relevant literature, concentrating on specific groups where releases of captive-bred individuals for reasons a-e above have been most common (excluding at this stage the literature on biological pest control). Thus, Sections III to VIII of the report consider the genetic aspects of releasing captive-bred species of freshwater fish, gamebirds, raptors, rodents and lagomorphs, deer, carnivores and Lepidoptera (mainly butterflies). Section IX discusses the special case of genetic interaction between domesticated and wild stocks of honey-bees, and Section X details the research at NERC's

Institute of Virology and Environmental Microbiology which is relevant to releasing microorganisms, specifically viruses, including those which may have been genetically manipulated.

Prior to these case studies, Section II reviews some general genetic and theoretical aspects of the problem and considers what can be learned from studies of hybridisation, usually between two natural populations.

The results of the studies reported in Sections II - X of this report are brought together and described in less technical language below. This, this section stands alone as a brief review of the findings to date, with some additional recommendations.

## 2 RESULTS

2.1 There is a dearth of studies of the genetic interactions between introduced and naturally-occurring individuals of the same or related species. Furthermore, where such interactions have been followed in detail they have usually involved organisms transferred from one natural population to another, not from captivity to the wild. Most studies of introductions have focused on the impact of the released individuals on native species through competition, predation, the spread of disease, or altering the habitat. Therefore, the problem of genetic interaction between captive-bred and naturally-occurring individuals has to be addressed largely by analogy with that which occurs between natural populations. In this respect, cases of deliberate or accidental introductions, and of hybridisation where populations have come into contact naturally, often following a period of separation, are particularly apposite.

2.2 Despite the lack of detailed studies, it is evident that genetic interactions between captive-bred and native individuals do occur, and may be particularly widespread among some groups such as freshwater fish, gamebirds, deer and certain outbreeding crop plants. Moreover, genes from introduced species can, in some circumstances, spread rapidly into native populations. In one of the genetically best-studied examples, genes from an introduced pupfish (minnow) species spread to occupy more than 400 km of river in less than five years by hybridisation with a native species. In another study, genes from an experimentally-introduced house mouse

population were found in mice throughout the small island (the Isle of May) to which they had been introduced only six months after release, including a site around 2 km away from the place of release.

2.3 It is also clear that genetic interaction between captive-bred and naturally-occurring individuals may have deleterious effects where it leads to a loss of genetic diversity. The extent and pattern of blending of genetic material between captive-bred and wild individuals depends on the fitness of the hybrids and their descendants. Hybrids carrying genes from captive-bred individuals may be less fit and, in most of the examples encountered, considerably less fit, than wild types. There are, however, notable exceptions, including several freshwater fish species. Furthermore, reduced hybrid fitness will not necessarily lead to their immediate elimination from natural populations, particularly where repeated hybridisations occur, as between crop plants and their wild relatives. Indeed, the fitness of an organism can be measured only over several generations. The high short-term fitness of, for example, introduced stocks of brown trout, may be in contrast to their reduced relative long-term fitness compared to the local population which has survived for many generations - and may contain genes which enhance its survival in conditions (e.g of disease or food shortage) not yet encountered by the hatchery fish.

Even where genetic diversity cannot be proved to have an adaptive basis, it is widely accepted as being a desirable feature of natural populations of animals and plants, and its maintenance is

acknowledged as a major goal of nature conservation. Such diversity may include the differentiation of local populations into genetically characteristic groups, sometimes containing rare genes or combinations of genes. The widespread release of captive-bred individuals is seen as posing a particular threat to the maintenance of this type of genetic diversity. The extent to which natural populations are subdivided into local populations with different genetic composition depends on a wide range of factors, including the mobility of the species, its breeding system, and its evolutionary history.

2.4 Despite studies of genetic interactions between natural populations, and the realisation of what may happen in specific cases, there appears to be a very poor base from which to make predictions about future releases. There is too much variation in the outcome of particular introductions to make confident generalisations. For instance, in the only other genetically-documented case of introducing house mice to an island (Gull Island), the introduced gene failed to spread and eventually disappeared from the population. Whether or not two populations will hybridise on contact, and the extent to which they will fuse genetically, is rather poorly understood. Ecological and behavioural factors play an important part in the spread of genes from an introduced population into that of a wild relative. For example, in the pupfish study quoted earlier, the rapid spread of genes from the introduced subspecies is believed to have been enhanced by native females preferentially mating with introduced males. Equally, the failure of the house mouse gene to spread

on Gull Island was partly attributed to social factors including the reluctance of local animals to breed with the introduced ones. Indeed, mating systems are likely to be of key importance, in both animals and plants, in determining the rates of gene flow between populations.

2.5 Theoretical population genetics provides useful models for considering genetic interactions between populations, but the many simplifying assumptions of such models demand that they are treated as metaphors and not used to attempt quantitative predictions. For example, the effects of different rates of gene migration can be evaluated theoretically to underline the idea that very low rates of gene flow between populations, equivalent in some cases to one migrant per population per generation, are sufficient to retain genetic similarity between populations. Similarly, it can be established that in certain circumstances a small release could have a large effect on genetic variation in the invaded population.



### 3 CONCLUSIONS AND RECOMMENDATIONS

3.1 Because evolutionary, ecological and behavioural factors can have an overriding impact on the genetic interactions between captive-bred and natural populations, it is imperative that each release is considered on a case-by-case basis. However, those features of the species' biology which have determined the pattern and rates of gene flow between natural populations in the past are likely to provide a useful guide to predicting the spread of genes from released populations in the future. Thus, the release of species in certain highly mobile animal groups, and in those animal and plant groups where a great deal of infertility is retained among widely separated populations, has a particularly large potential impact on natural populations.

3.2 Protocols for introducing captive-bred species are likely to vary between species and will need to be formulated with the ecology and evolutionary history of each species in mind (as for example in the code of conduct for re-establishing insect populations, drawn up by the Joint Committee for the Conservation of British Insects - see Section VIII). The conclusions to Section III of this report give detailed recommendations for the release of captive-bred freshwater fish, particularly brown trout and salmon. Although the protocols may vary between species, it should be possible to pose a series of standard questions about each release which characterise the organism and the environment into which it is to be released, and hence enable a 'risk assessment' of genetic interaction. Some of these questions, which relate to the geographic range, the range of

habitats, the fitness, mobility and trophic interactions of the organism, and the isolation, patchiness, diversity, and sensitivity of the environment (including the presence of relatives), have been considered in attempts to design risk assessments for the release of genetically-modified organisms. It is not inappropriate, when planning to release captive-bred individuals for nature conservation or game-stocking purposes, to adopt a level of caution similar to that for releasing genetically-modified organisms.

3.3 That the release of genetically-manipulated organisms may constitute a particular problem has been widely recognised in the scientific community, and thus concern is being reflected at public level, for example in the 13th Report of the Royal Commission on Environmental Pollution (The Release of Genetically Engineered Organisms to the Environment, HMSO, July 1989) and the recent Environmental Protection Bill (1989), Clauses 83-97. Guidelines for the introduction of such organisms have been in place for some time (e.g. the joint AFRC/HSE guidelines on the use of transgenic animals). Ecologists have been involved in considering these problems and the ecological perspective is covered in several publications (e.g. The Ecological Society of America (ESA) workshop publication in Ecology (1989), Volume 70, pages 298-315). Many of the conclusions reached in these reports apply equally to the release of captive-bred species which have not been genetically engineered by modern technology, such as micro-injection, protoplast fusion or recombinant DNA techniques. They similarly reflect some of the key uncertainties. For example, the ESA paper

concludes that "Many engineered organisms will probably be less fit than the parent organism, although some important exceptions may arise." Such highly qualified statements have also to be made about releasing captive-bred species, reflecting the gaps in our understanding of the effects of captivity on fitness and natural selection in changing environments.

- 3.4 Among the major gaps in our understanding are those in the areas of the effects of captivity on fitness, the dispersal of species and genes from their release points, and the constraints to reproductive interaction. Some weak generalisations exist in these areas - for example, fitness tends to decrease with the number of generations of captive breeding, and reproductive isolation tends similarly to increase with the period of time over which populations are separated. Dispersal and migration is well-understood in some groups and has been taken into account when releasing animals in areas from where they have been lost (e.g. the peregrine falcon in south-east USA, the large blue butterfly in England). However, the planning and monitoring of every release will need to raise questions about the effects of captivity, gene dispersal, and interaction with wild relatives. In particular, the pattern of suitable habitat for populations of the released species will need to be known: Does it occur in patches in the countryside? Are there corridors of suitable habitat connecting existing populations? How does the dispersal pattern of a particular species affect the chances of interacting with local populations (e.g. do males disperse, as in some deer? Is the pollen wind- or animal-dispersed?)? At our present level of

knowledge, each question has to be addressed on a case-by-case basis, as do the appropriate parameters to consider in planning and monitoring a particular introduction.

3.5 Recent advances in molecular genetics have provided an opportunity to monitor the genetic exchange between released individuals and those occurring in the wild. For many groups of higher organisms the ability to characterise the variation in their DNA by the range of techniques collectively referred to as 'genetic fingerprinting' offers the chance to monitor the fate and spread of genes in the wild. In many cases of releases in groups such as fish, birds or mammals, such genetic fingerprinting involves a relatively simple protocol, i.e. a small sample of blood being taken for each released animal. It is suggested that where captive-bred individuals belonging to such groups are released for nature conservation purposes, genetic fingerprinting is used to monitor the future genetic interactions between released and wild individuals.